

APPROVED	C.E. FIG.
BY	PASS SUBCLASS
DRAFTSMAN	

1/26

CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC TCA GCT GCT GTG GTG CTG ATG GIG CTG AGC AGC CCA AGG
 M A L Q I P S L L S A A V V L M V L S S P R
 KOZAK _____
 CONSENSUS

ACC TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT GAA ATC AAC GAA GCT GGT CGT
 T L S ↑ I S Q A V H A A E I N E A G R
 PEPTIDE LINKER _____ OVA 323-339 PEPTIDE

GCT AGC GGA GGG GGC GGA AGC GGC GGA AAC TCC GAA AGG // AGC CCC ATC ACT GTG GAG TGG
 A S G G G S G G G N S E R // S P I T V E W
 PEPTIDE LINKER _____ [aa1 IA^d β1-β2 DOMAINS aa189]
 SINGLE CHAIN LINKER

ACT AGT GGT GGC GGT AGC GGC GGT GGT GGT TCC GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCG AGT
 T S G G G S G G G S G G G S G G G S G G G S S
 PEPTIDE LINKER _____ SINGLE CHAIN LINKER

GAA GAC GAC ATT // CCA GGG CCT TTA TGA
 E D D I // P G P L •
 aa1 IA^d α CHAIN STOP

FIG. 1

APPROVED	O.G. FIG.
BY	ASS SUBCLASS
DRAFTSMAN	

2/26

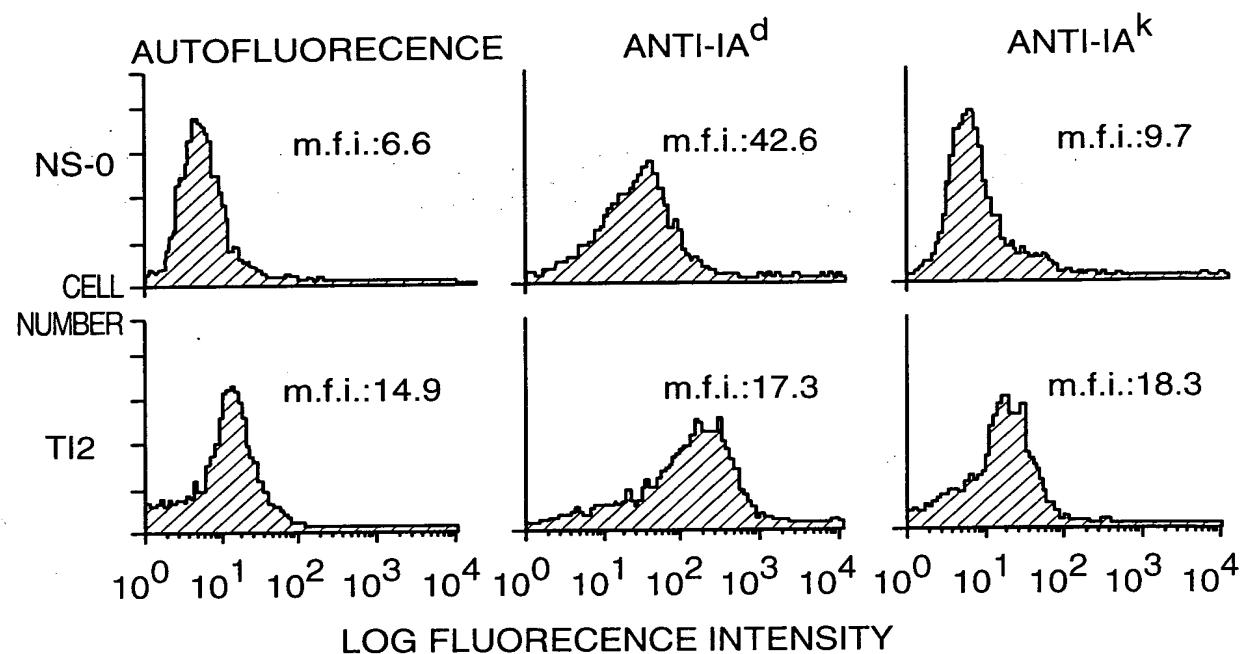


FIG. 2A

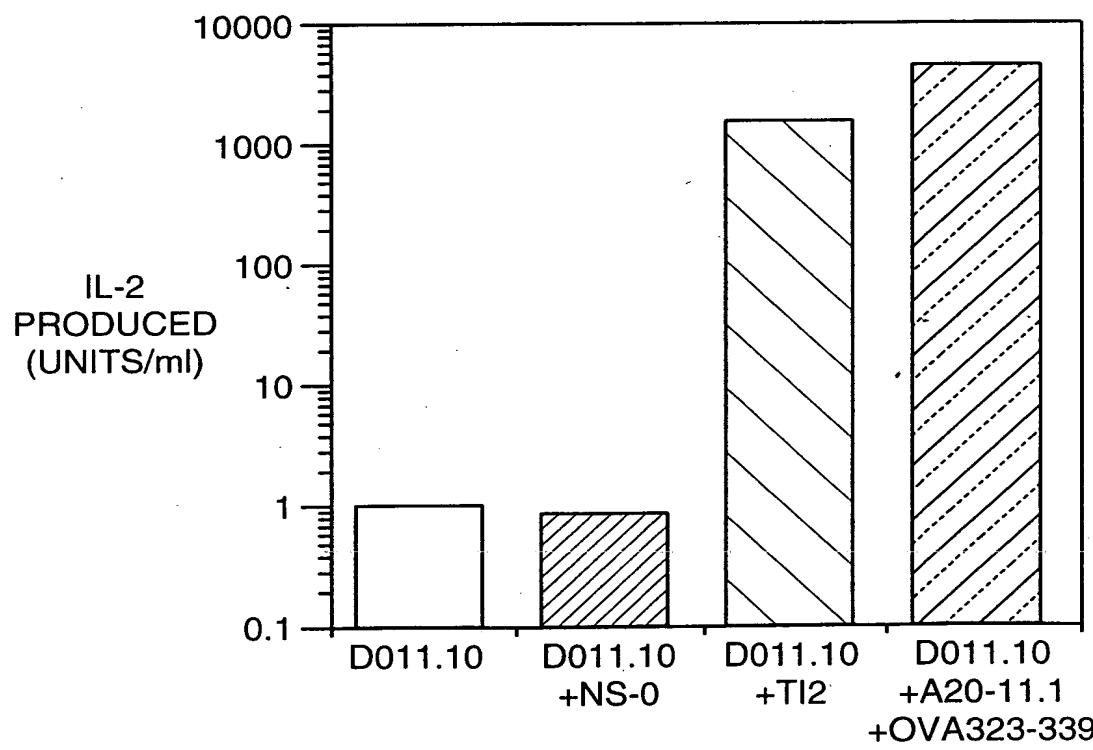


FIG. 2B

APPROVED	G.C. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

3/26

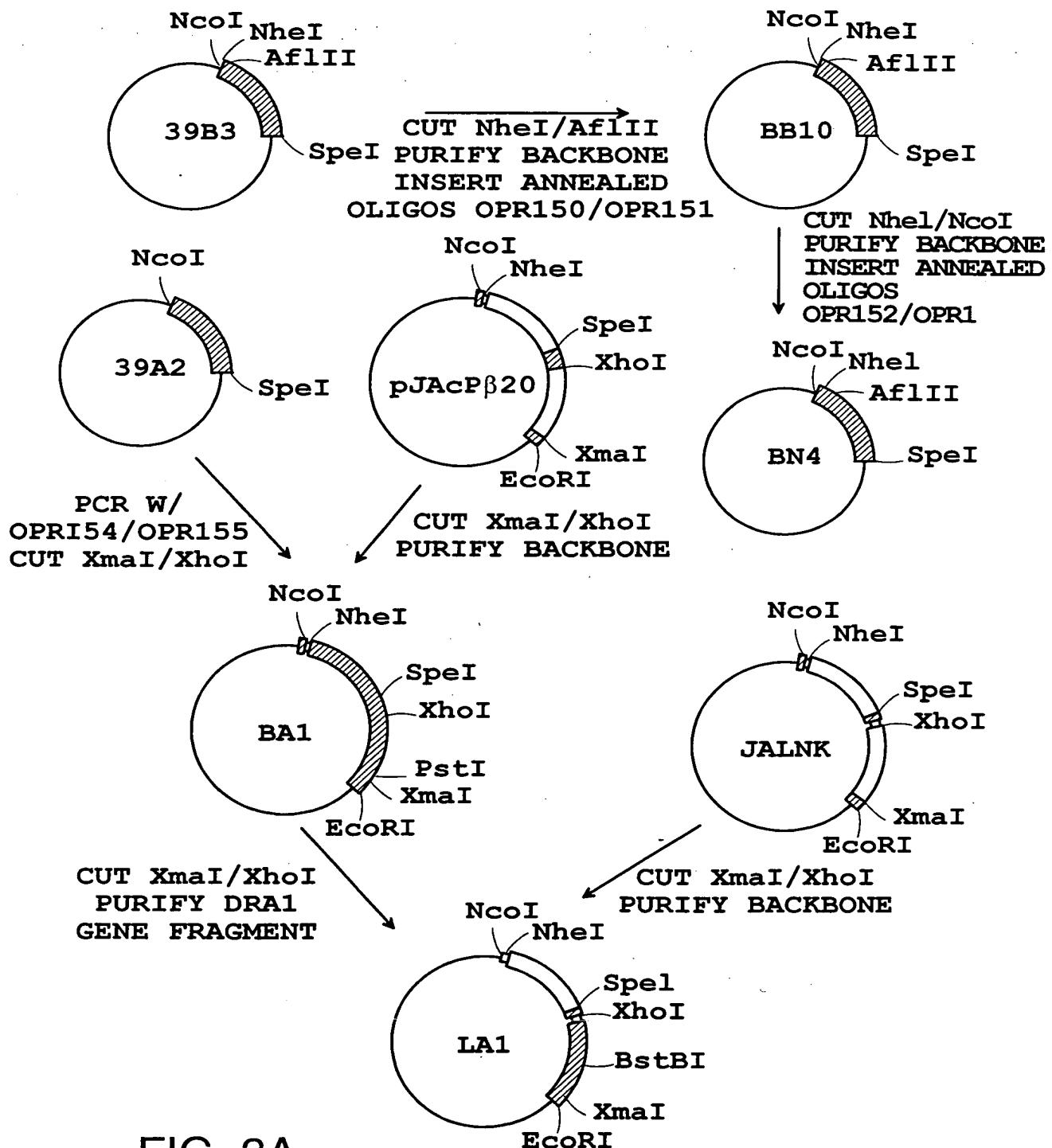


FIG. 3A

4/26

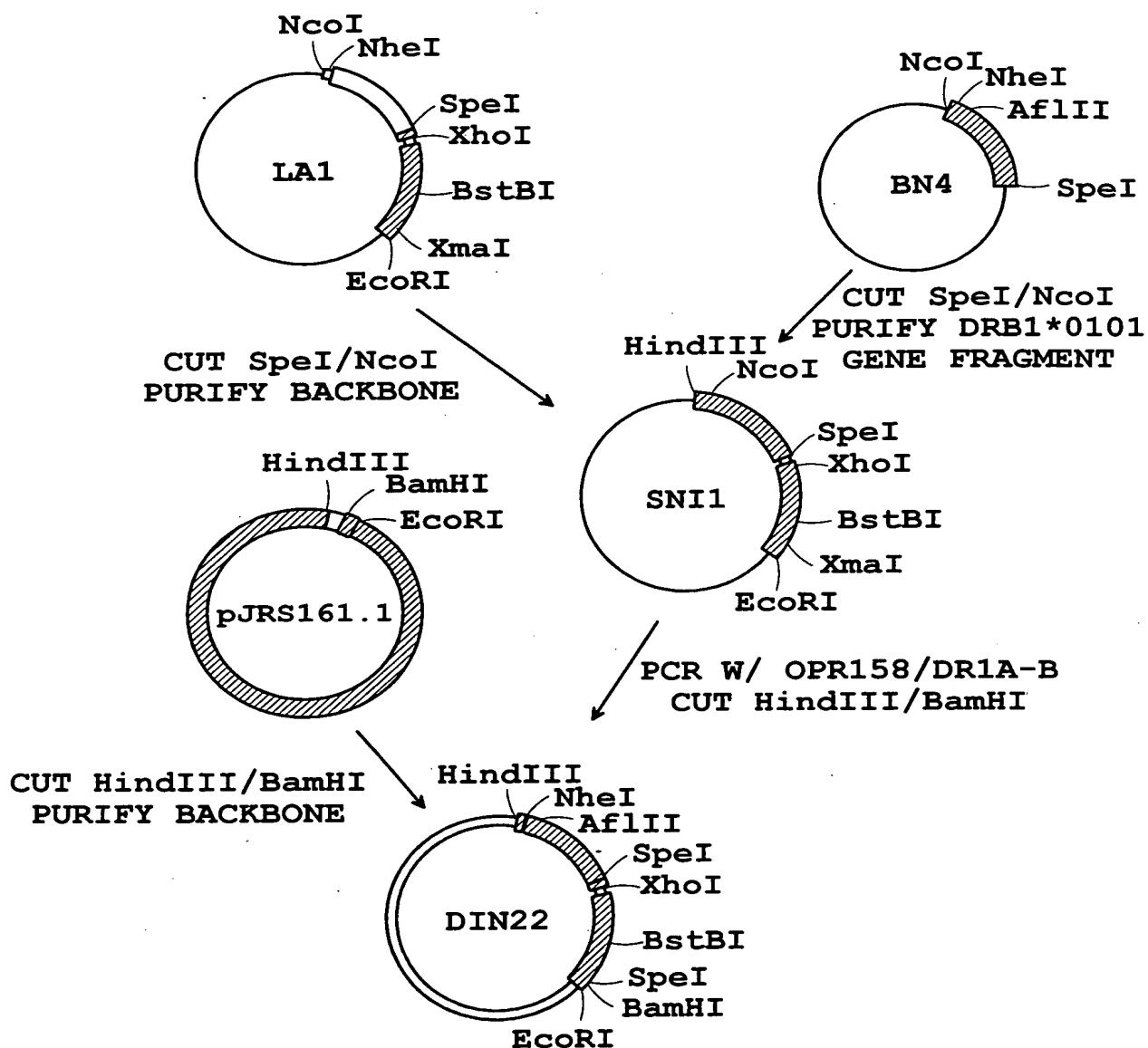


FIG. 3B

APPROVED	C.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

5/26

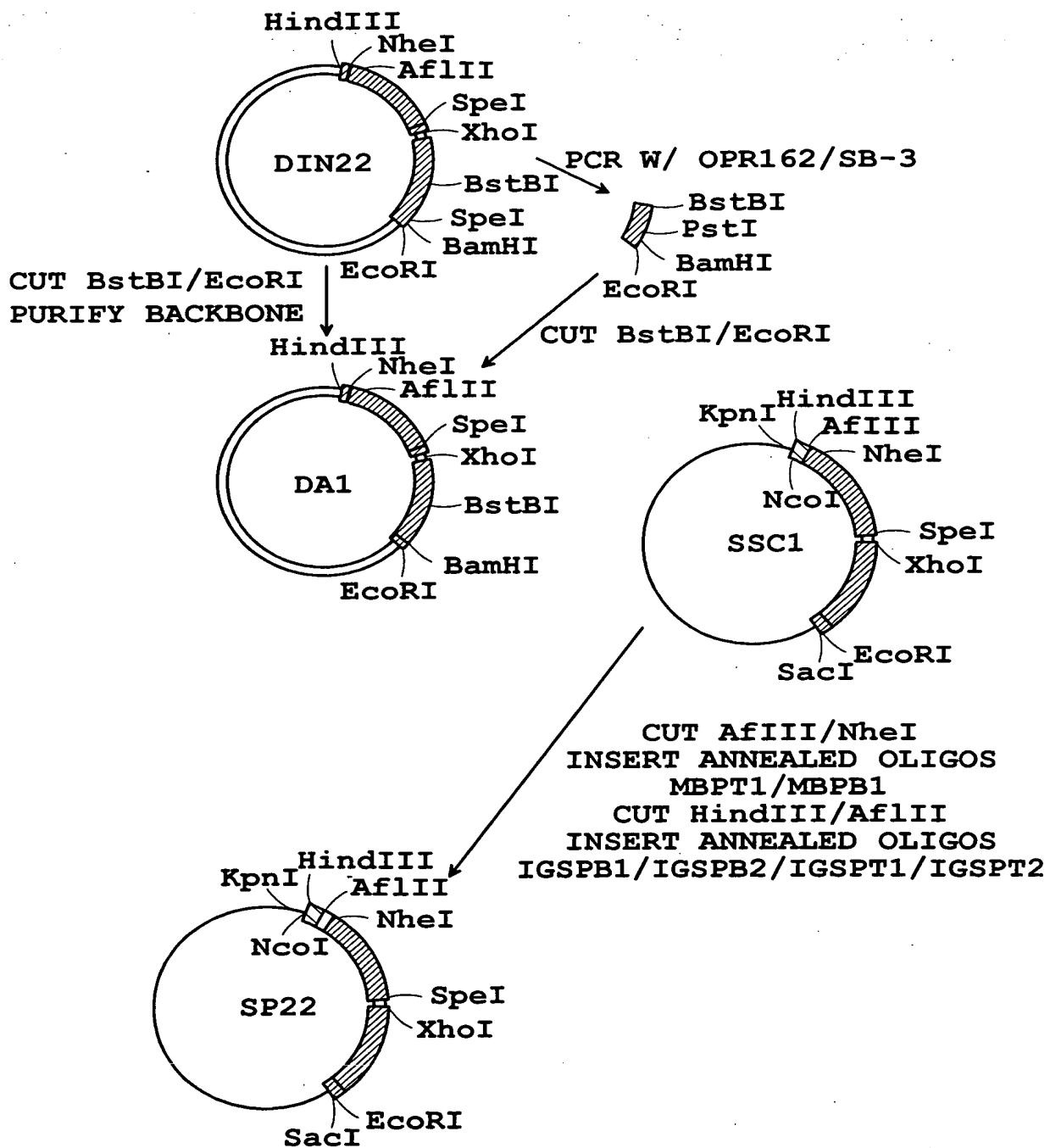


FIG. 3C

APPROV'D	1.8. FIG.
BY	ASS SUBCLASS
DRAFTSPRINTER	

6/26

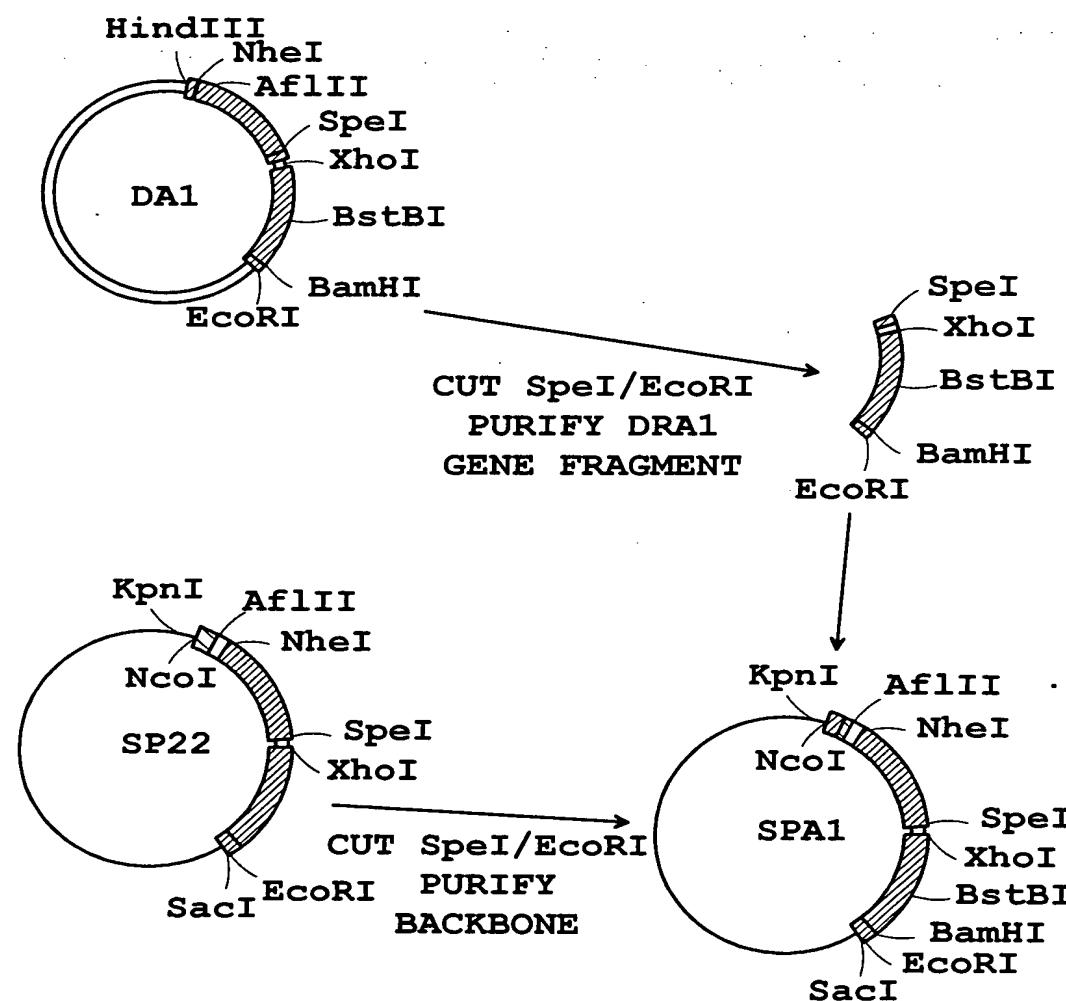


FIG. 3D

APPROVED	10.6 FIG.
FY	1985 SUBCLASS
DRAFTS 100	

7/26

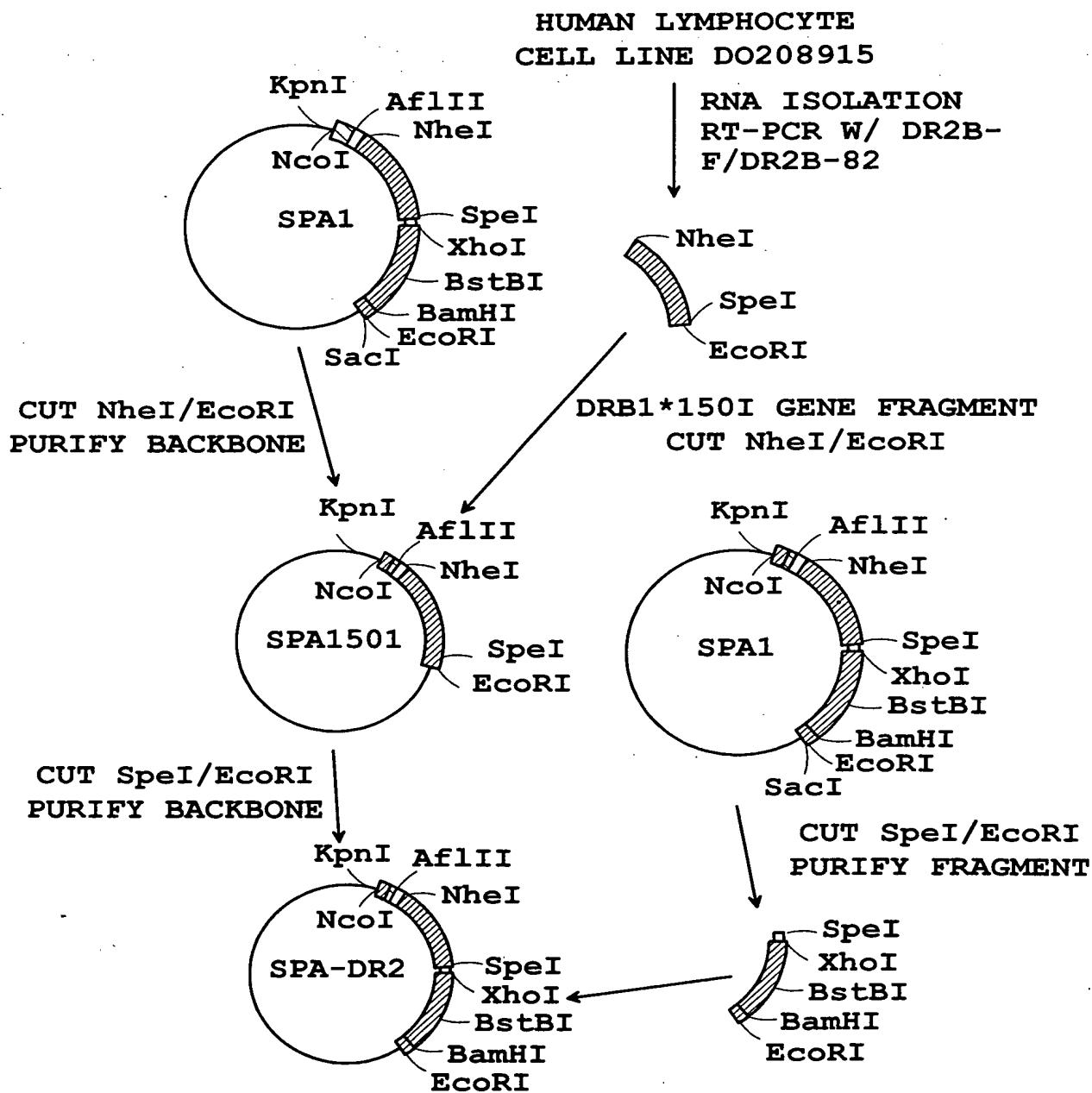
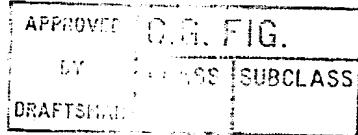


FIG. 3E



8/26

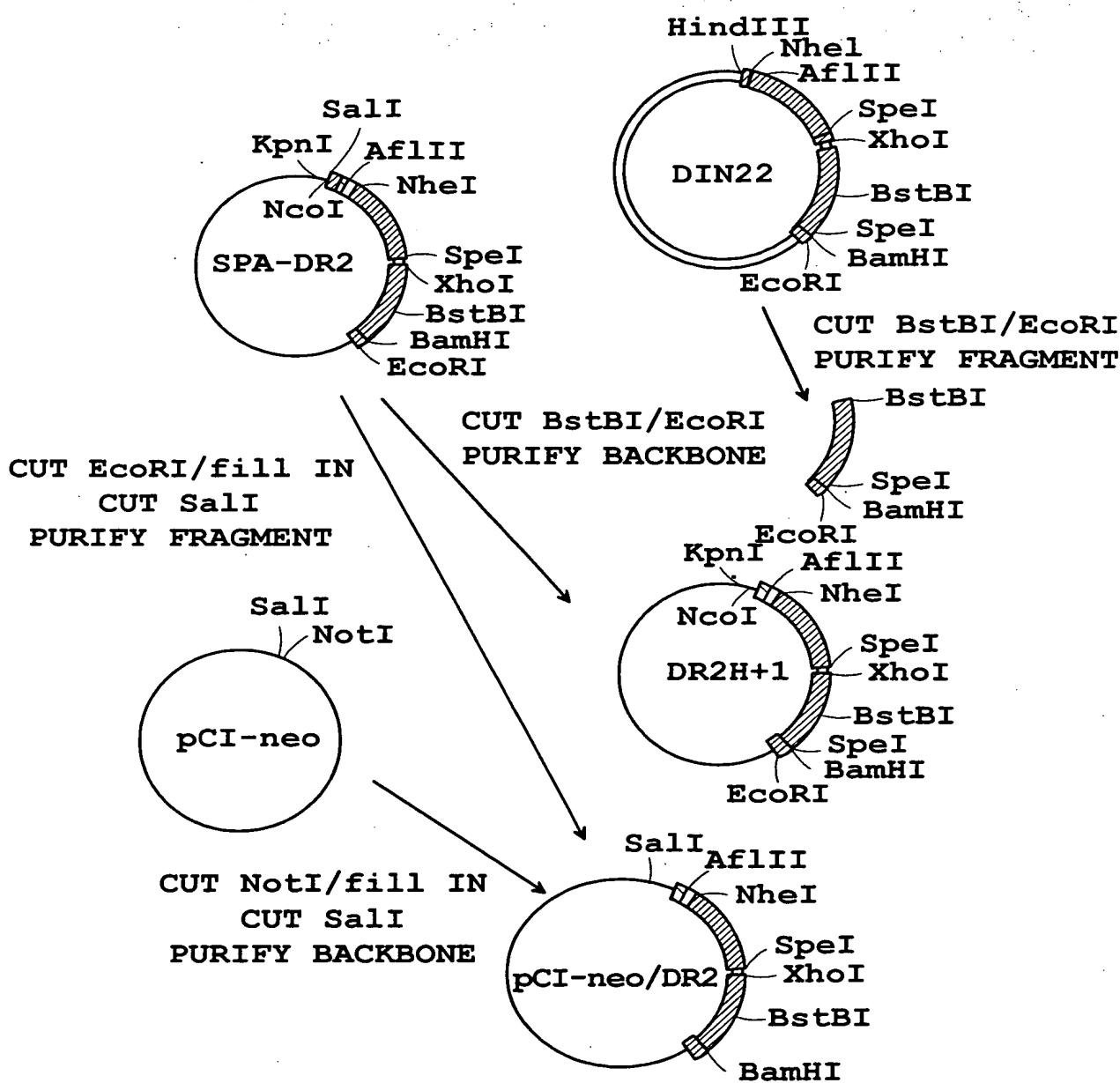


FIG. 3F

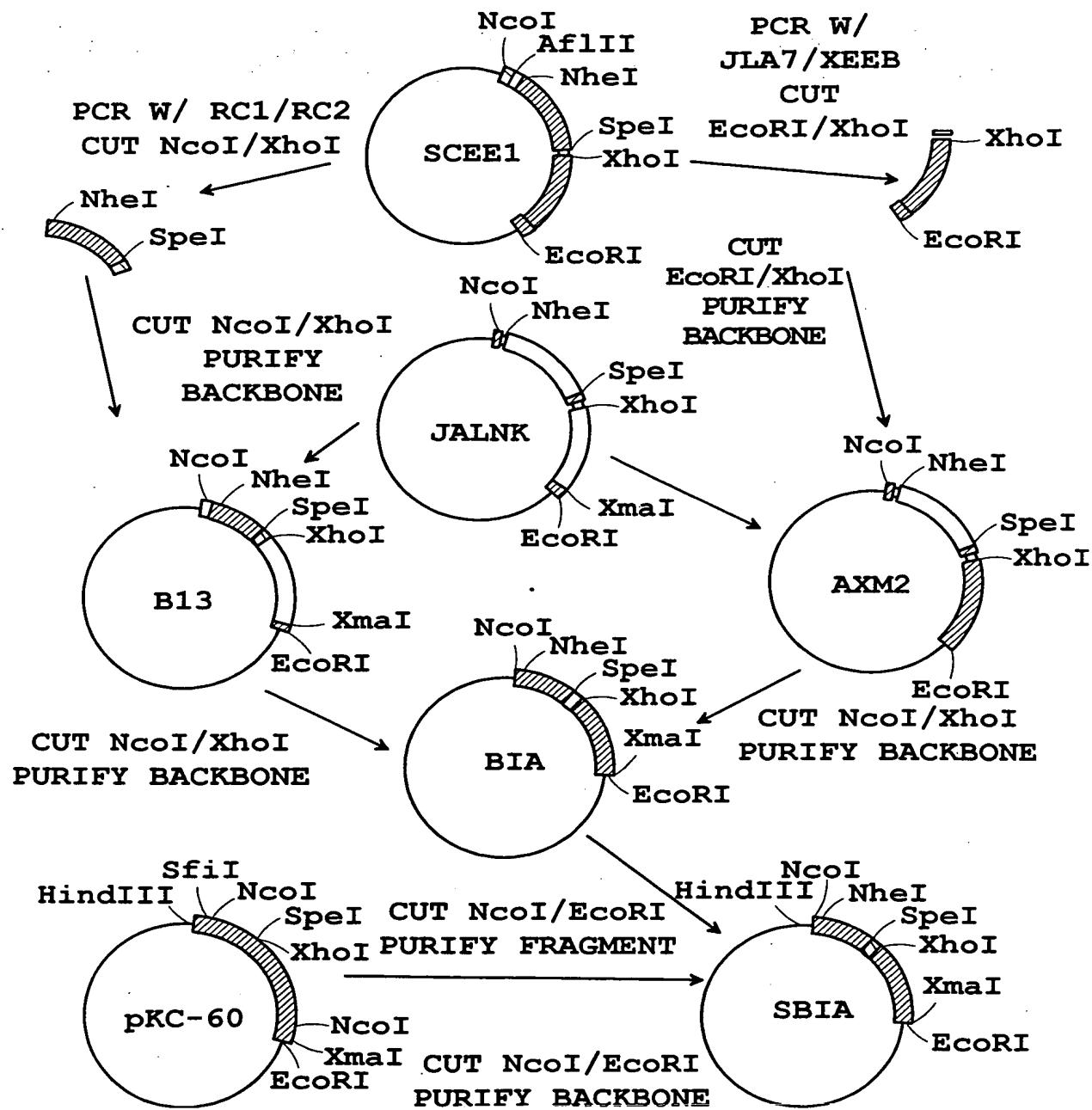


FIG. 3G

10/26

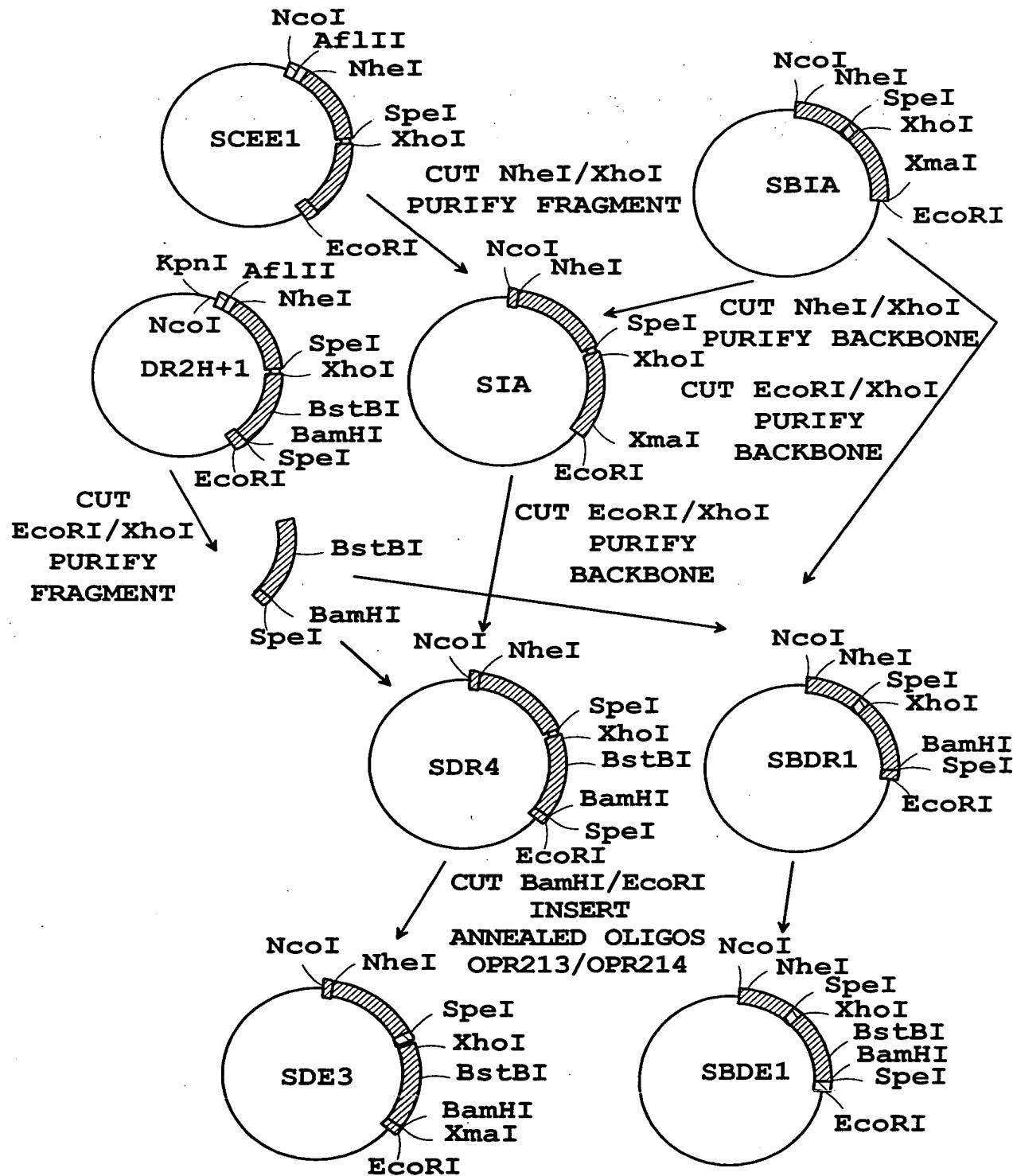


FIG. 3H

11/26

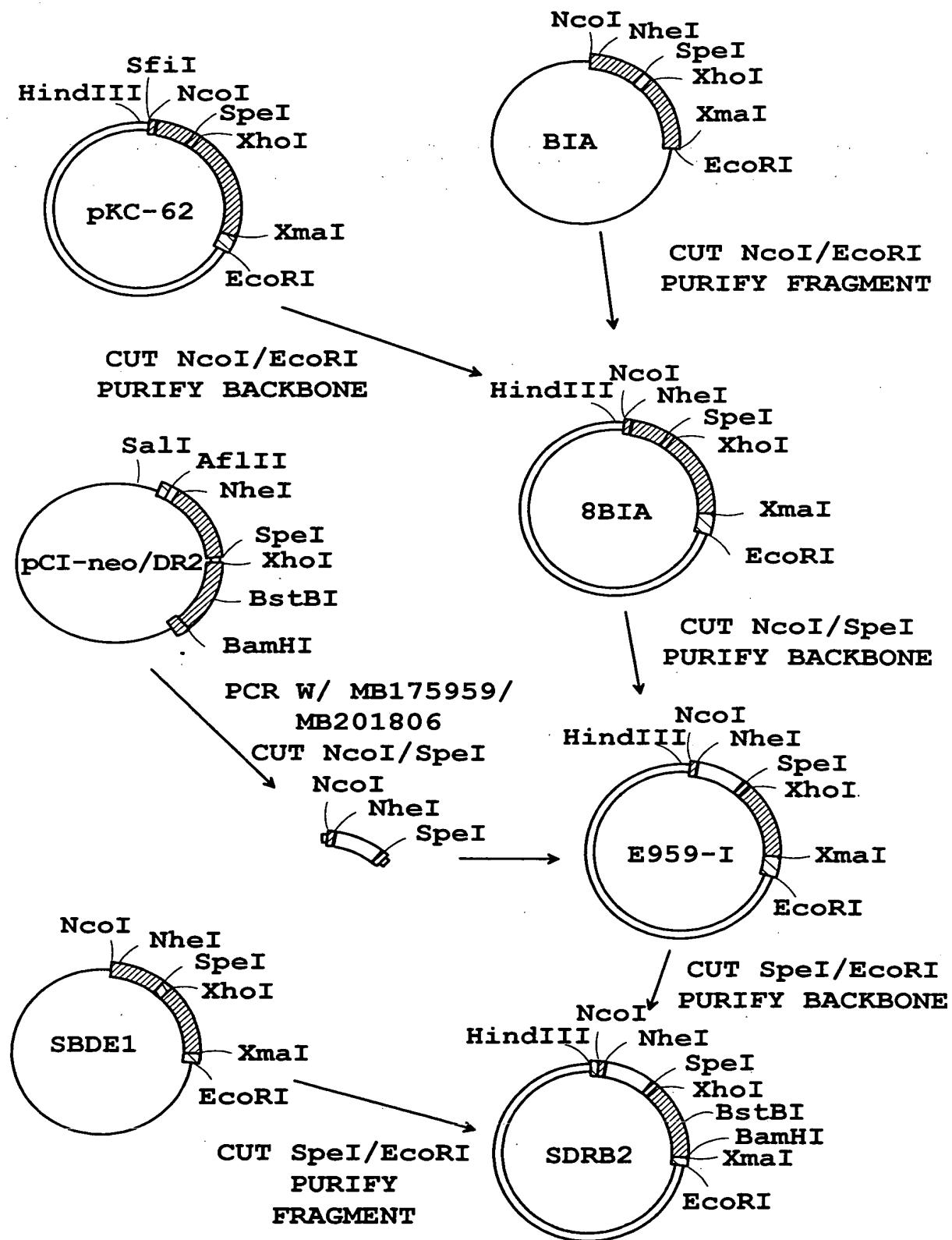


FIG. 3I

12/26

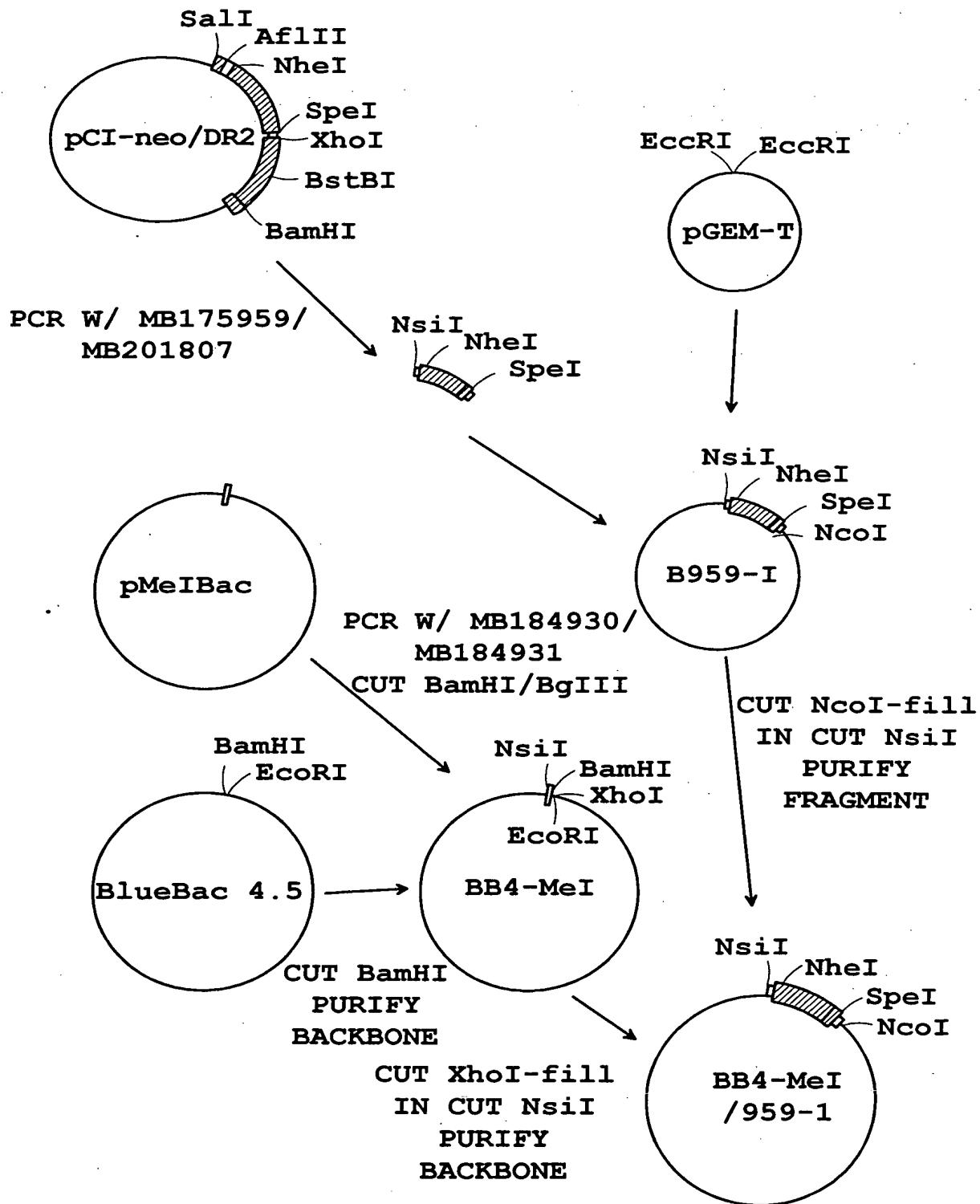


FIG. 3J

13/26

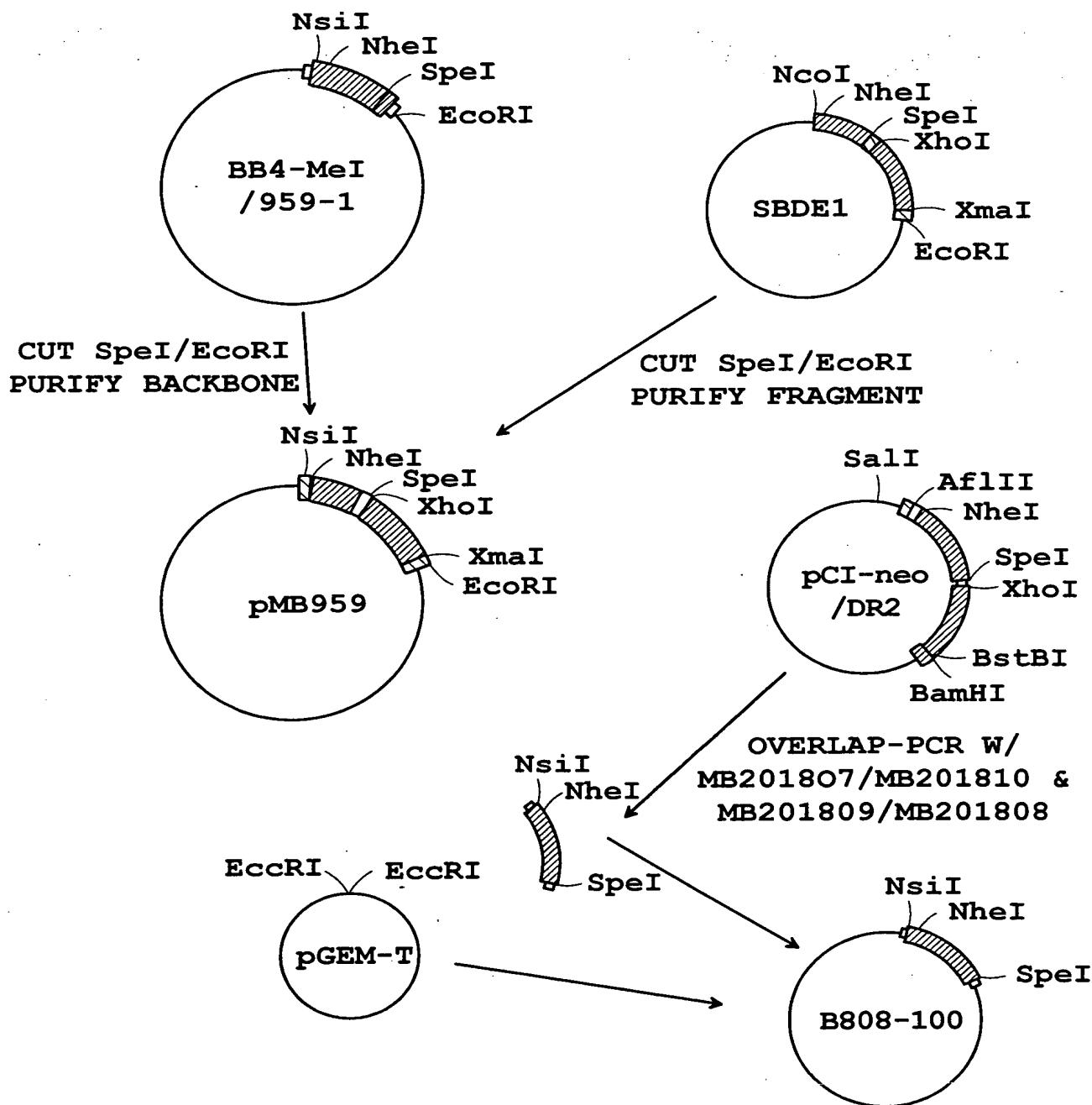


FIG. 3K

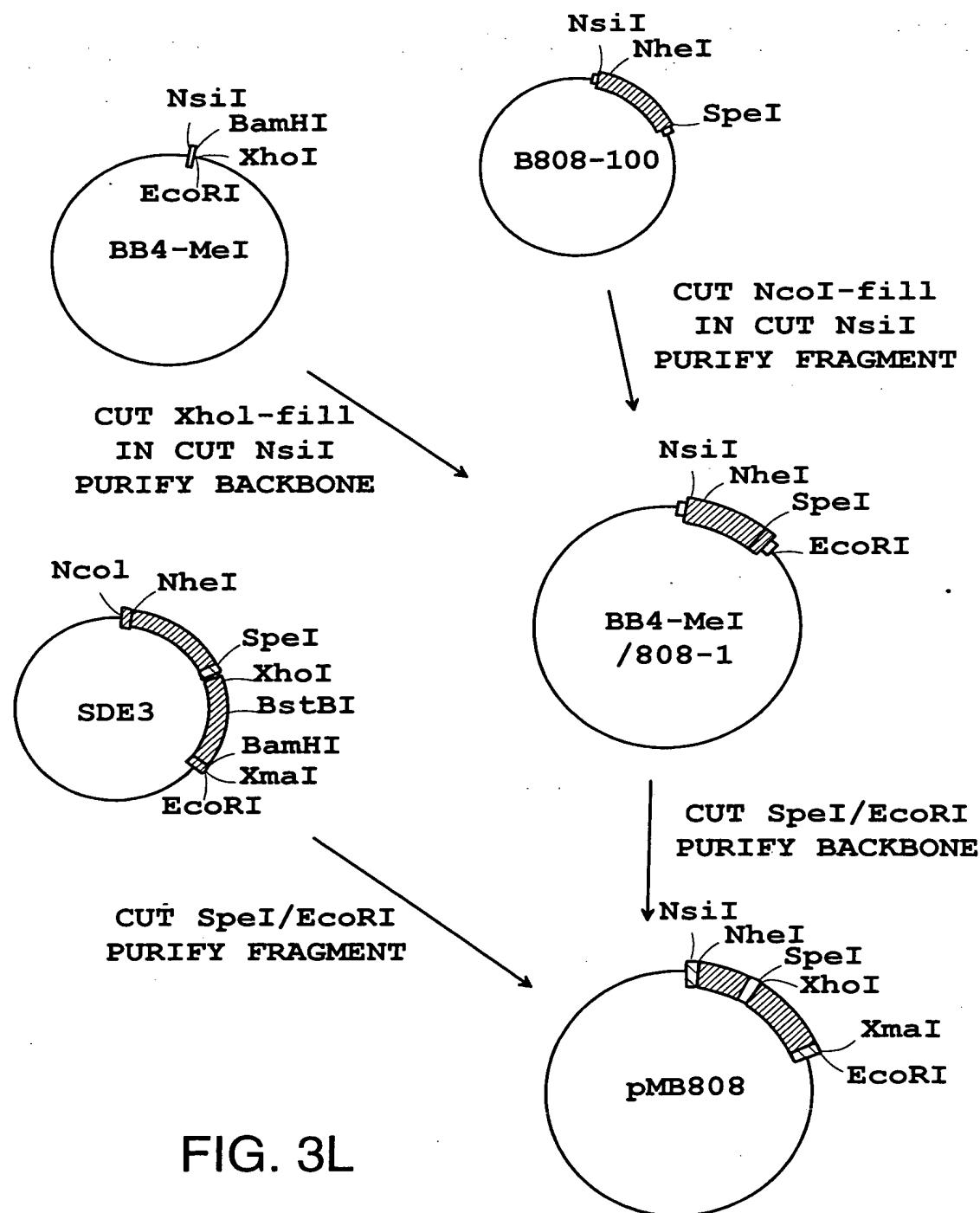


FIG. 3L

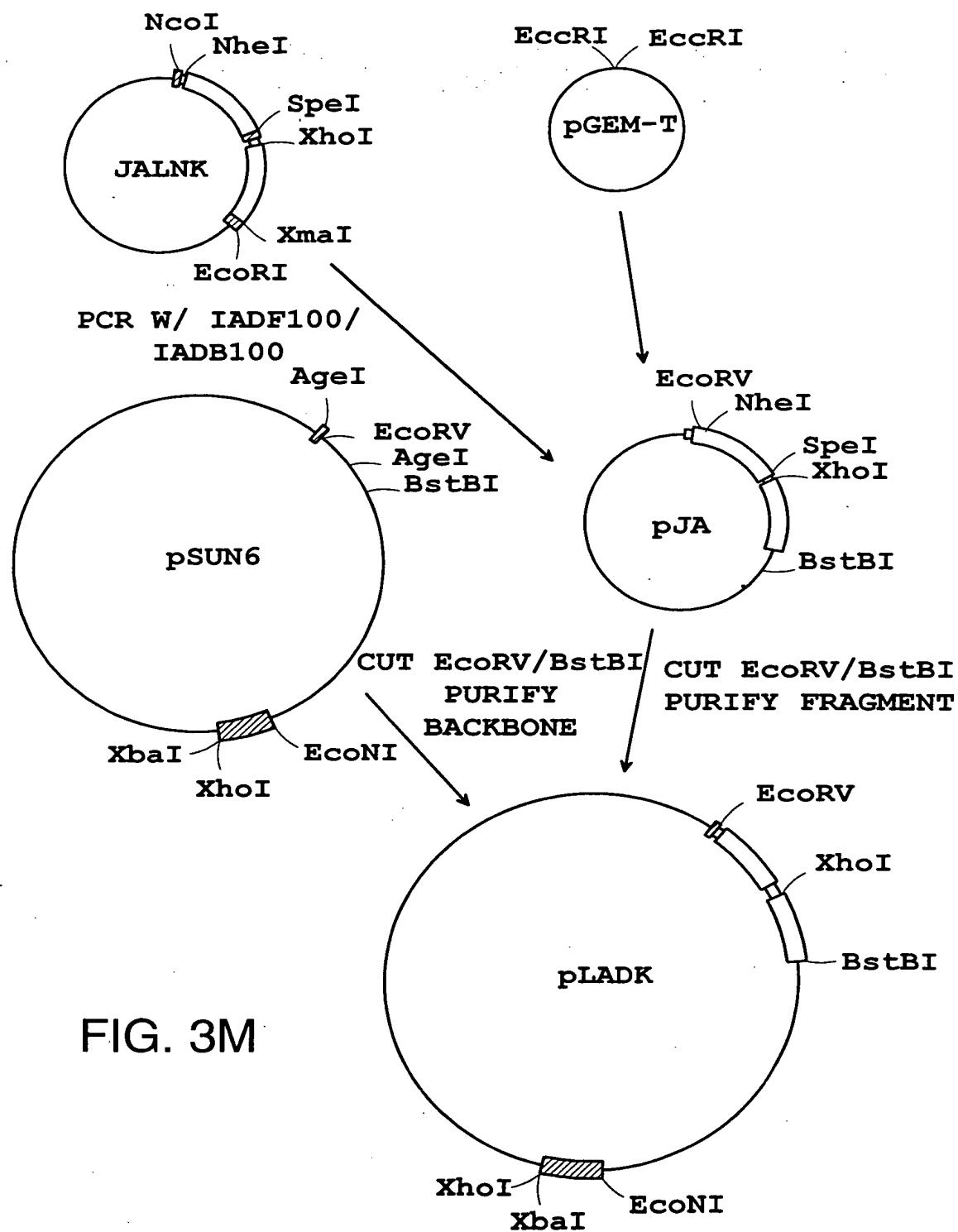
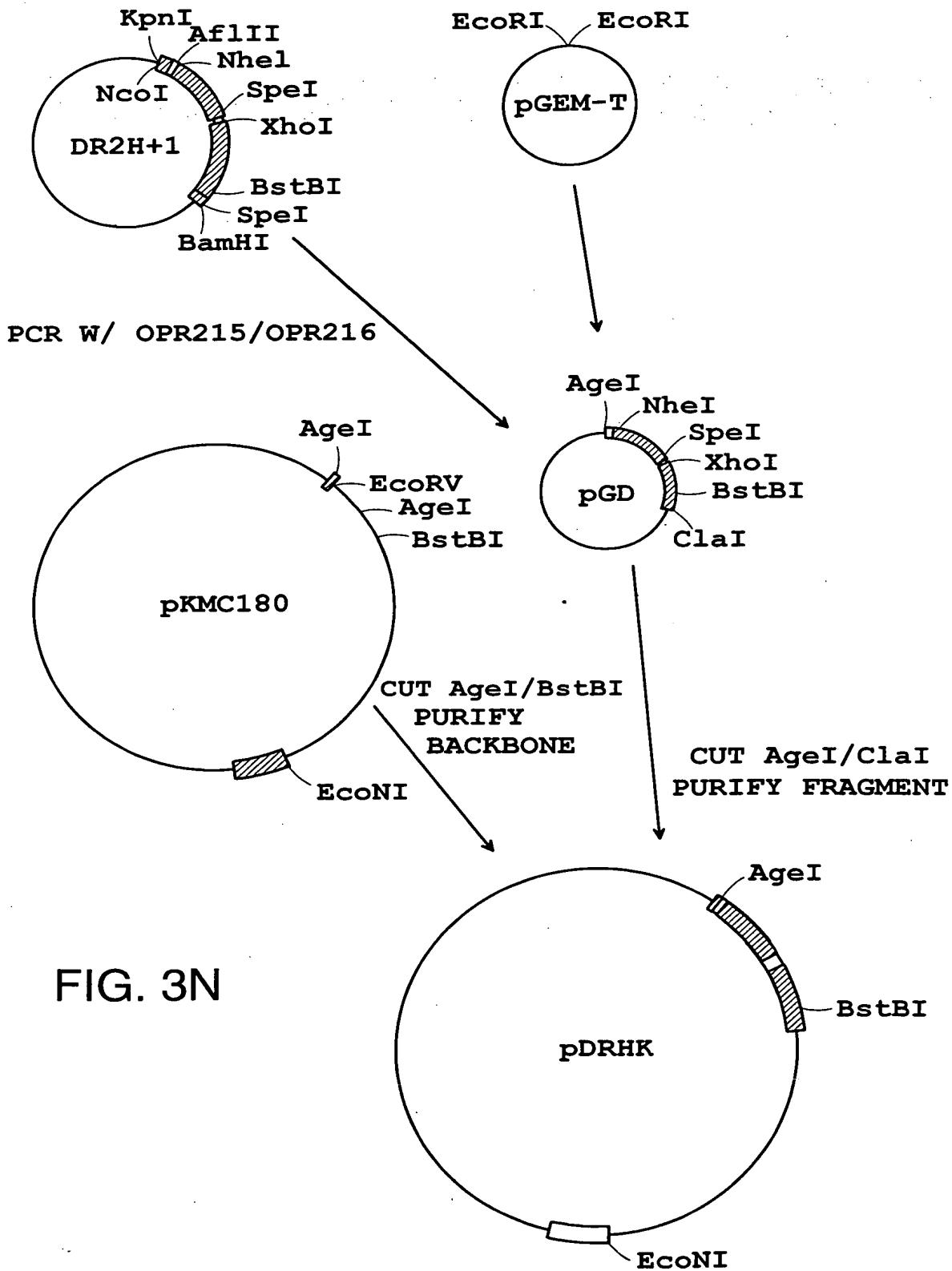


FIG. 3M



17/26

FIG. 4A

sc-1A ^d /PEPTIDE FUSION			
[SP]	PEP	L1	A ^d β1-β2
[SP]	PEP	L1	A ^d β1-β2
[SP]	PEP	L1	A ^d α ^{1-α²} EE

sc-1A^d/PEPTIDE FUSION

[SP]	PEP	L1	A ^d β1-β2
[SP]	PEP	L1	A ^d α ^{1-α²}

sc-1A^d/PEPTIDE-C_L FUSION

[SP]	PEP	L1	A ^d β1-β2
[SP]	PEP	L1	IgG C _L

sc-DR2/PEPTIDE-TAG FUSION

[SP]	PEP	L1	DRB1*1501 β1-β2
[SP]	PEP	L1	EE

sc-DR2-β²/PEPTIDE FUSION

[SP]	PEP	L1	DRB1*1501 β1
[SP]	PEP	L1	EE

sc-DR2 MOD β²/PEPTIDE FUSION

[SP]	PEP	L1	DRB1*1501 β1 MOD β2
[SP]	PEP	L1	EE

sc-DR2/PEPTIDE-C_L FUSION

[SP]	PEP	L1	DRB1*1501 β1-β2
[SP]	PEP	L1	IgG C _L

FIG. 4B

APPROVED
C.G. FIG.
BY CLASS SUBCLASS
DRAFTSHP

18/26

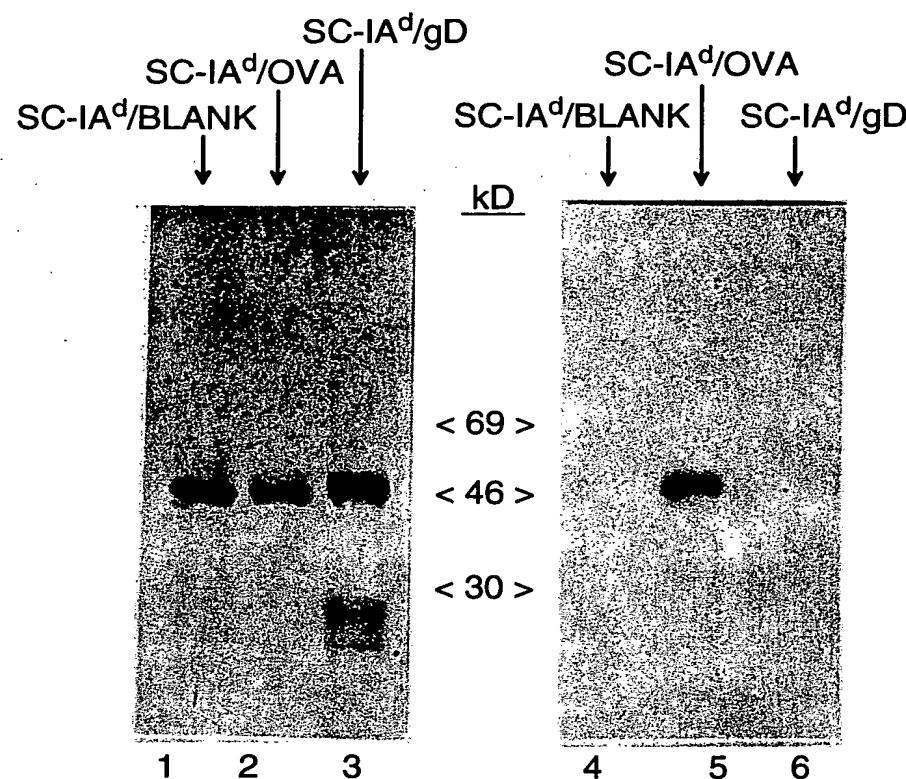


FIG. 5A

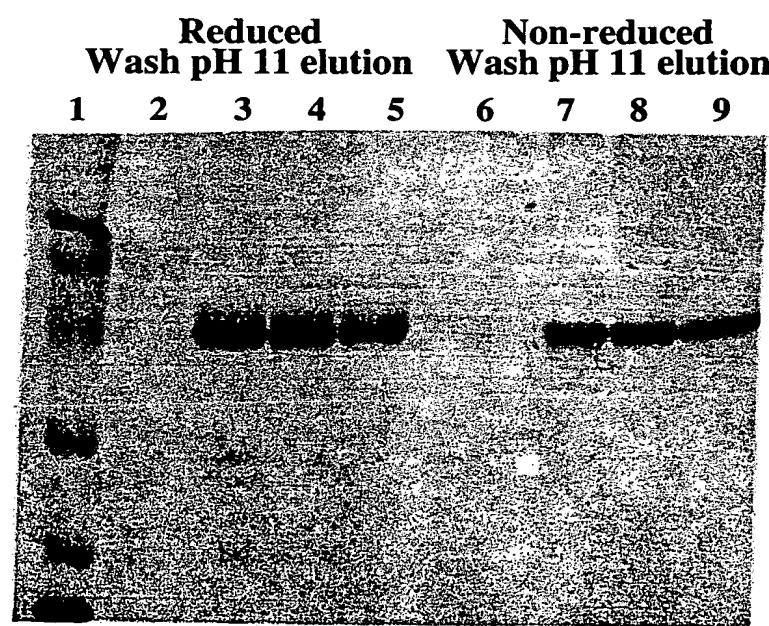


FIG. 5B

19/26

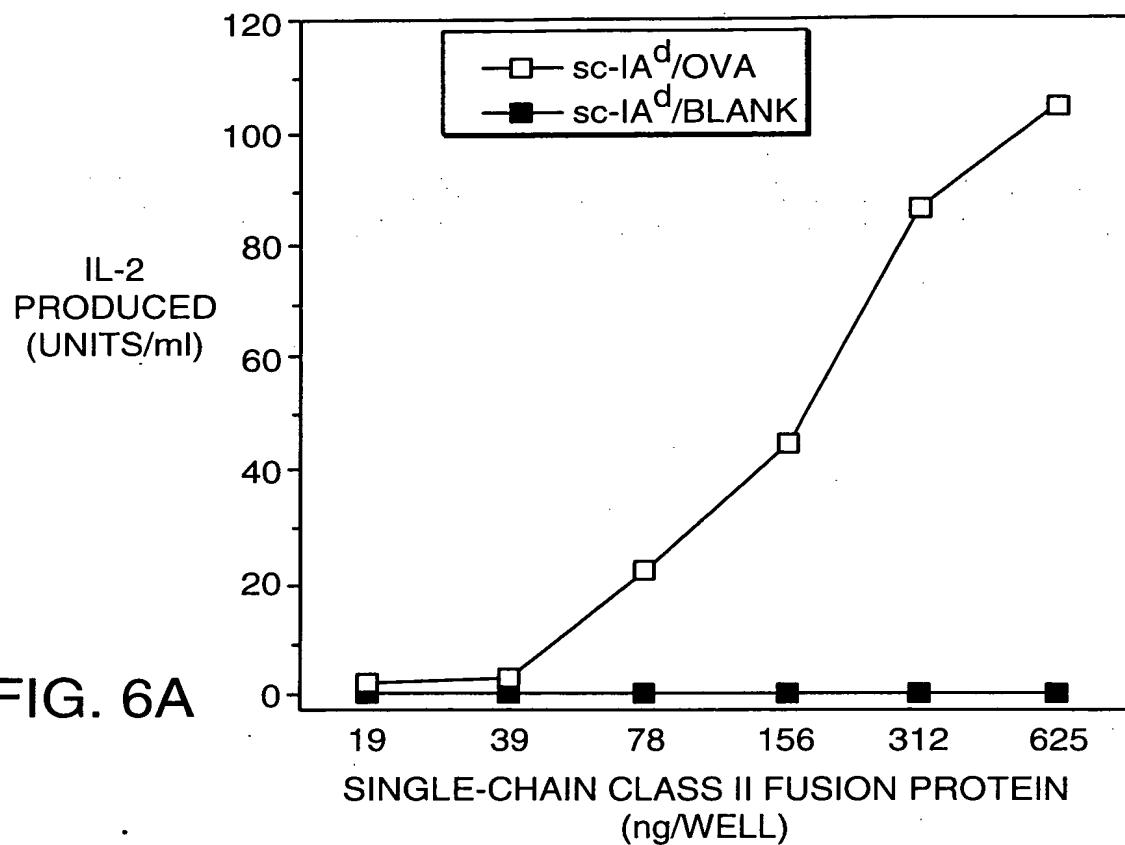


FIG. 6A

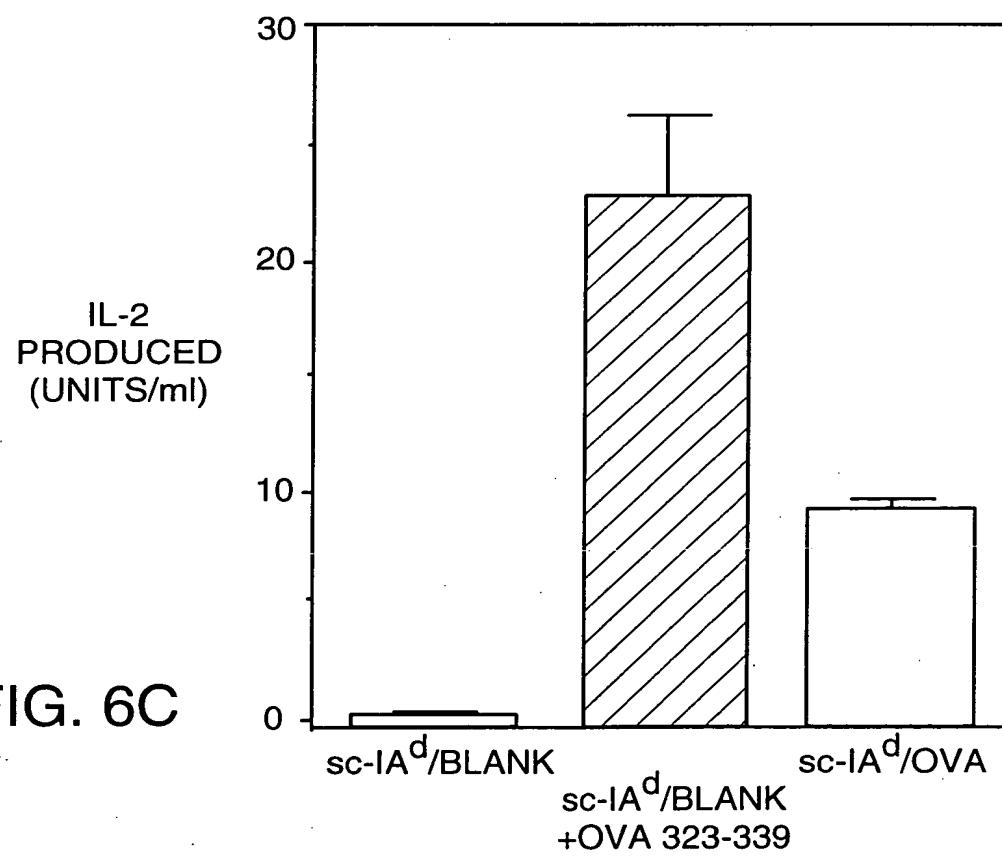


FIG. 6C

20/26

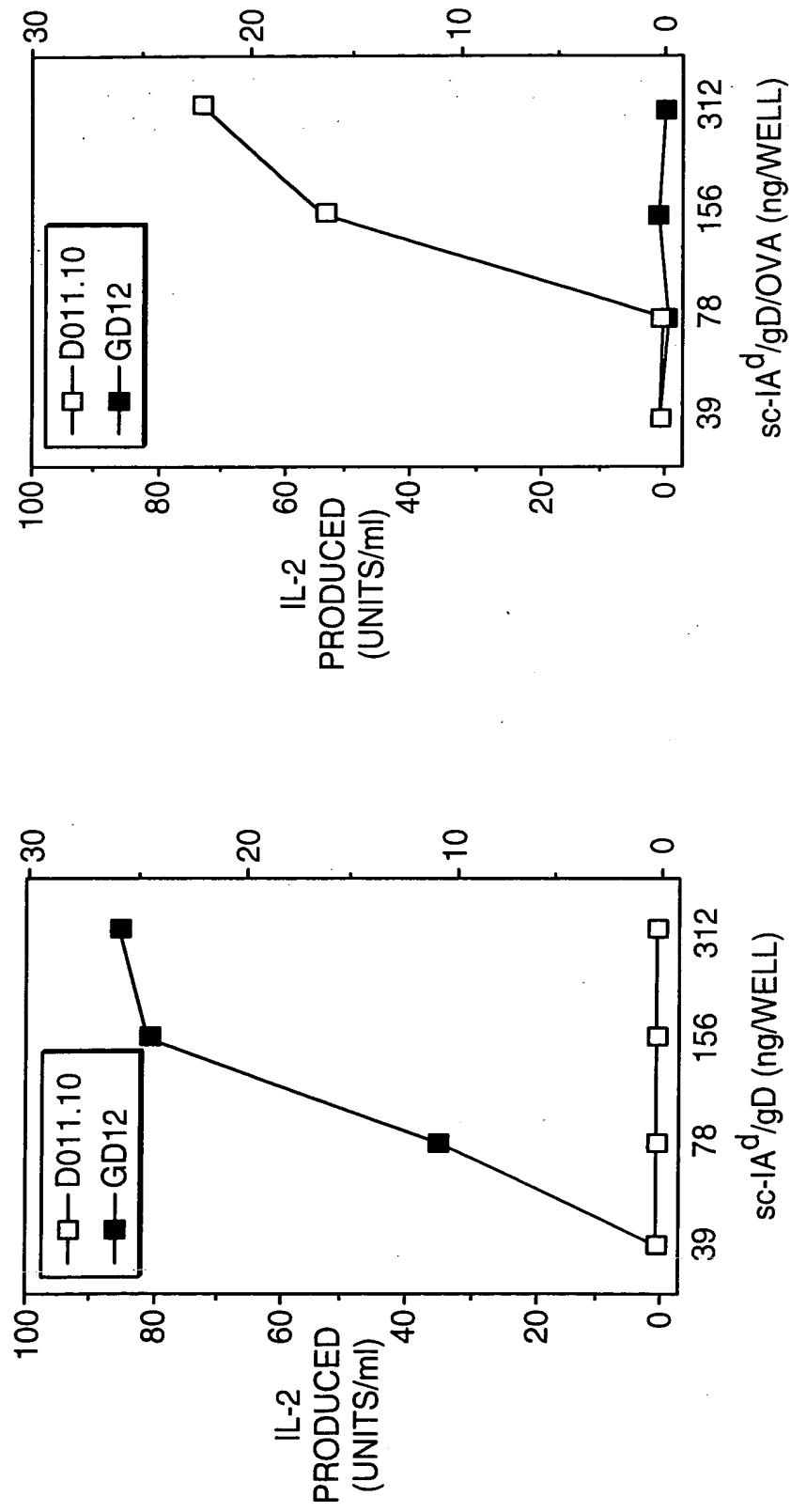


FIG. 6B-1

FIG. 6B-2

APPROVED	BY	FIG.
CLASS	CLASS	SUBCLASS
DRAFTSMAN		

21/26

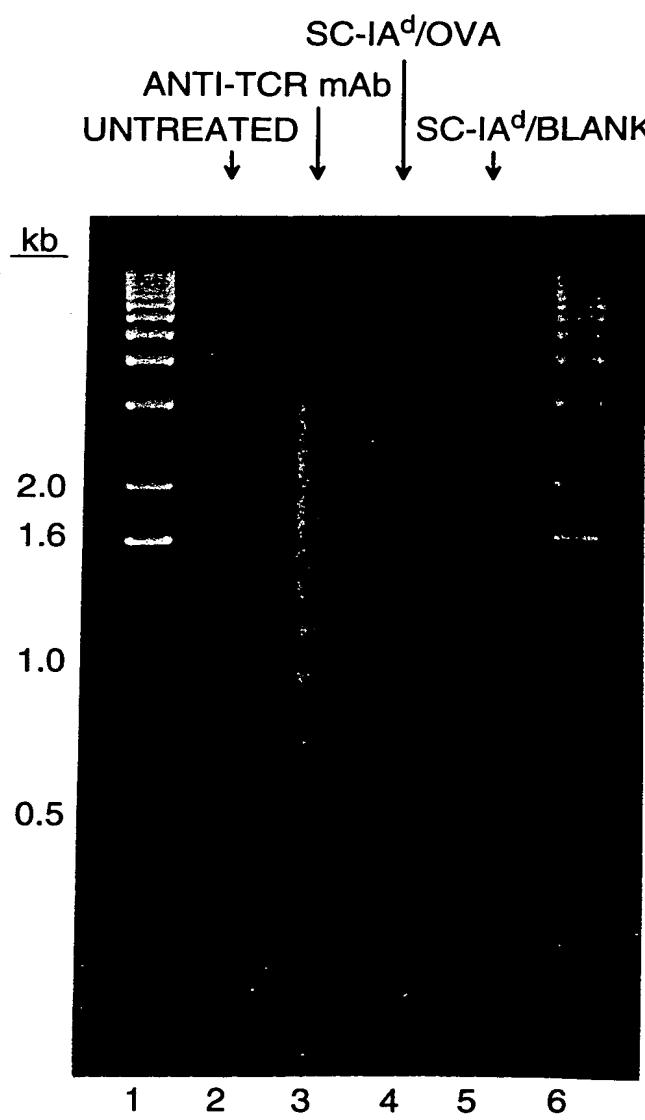


FIG. 7

APPROVED	BY	G. G. FIG.
	BY	CLASS SUBCLASS
DRAFTSMAN		

22/26

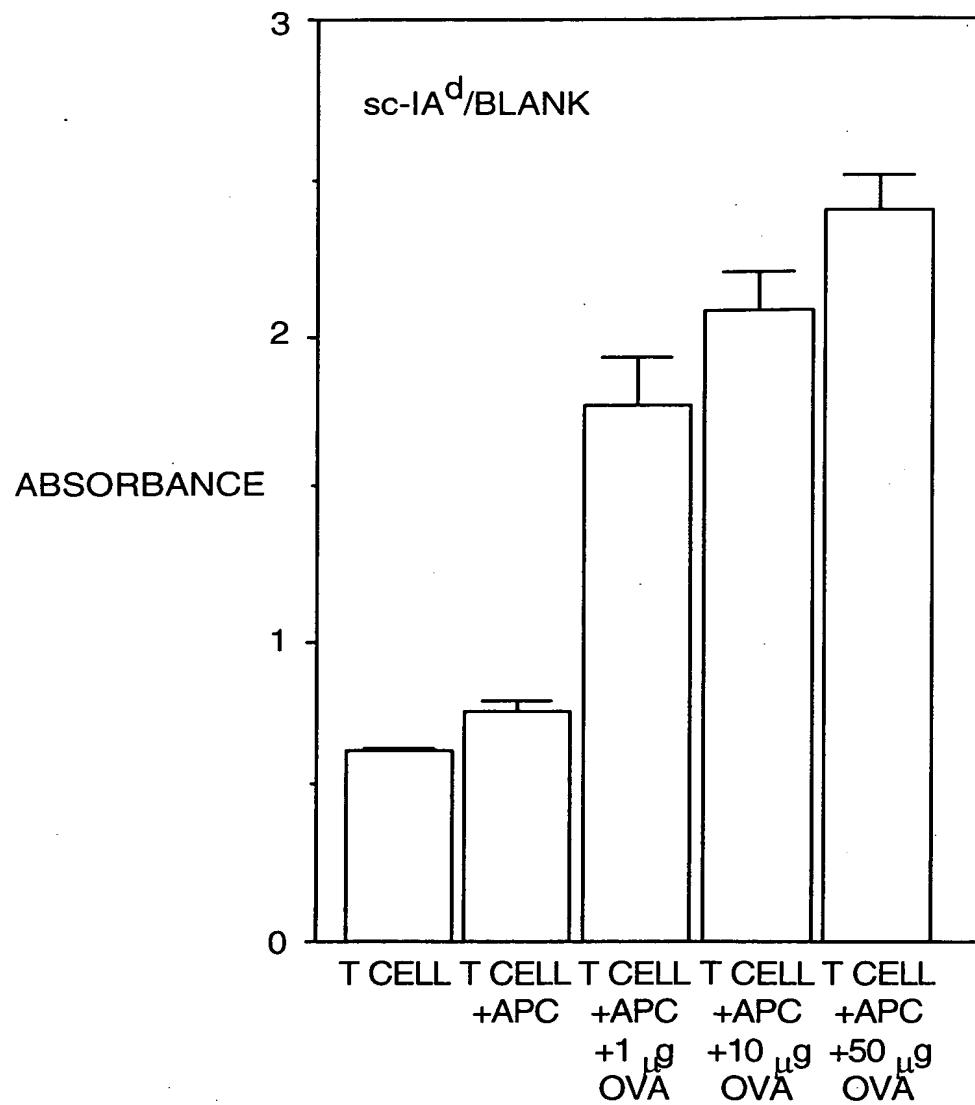


FIG. 8A

23/26

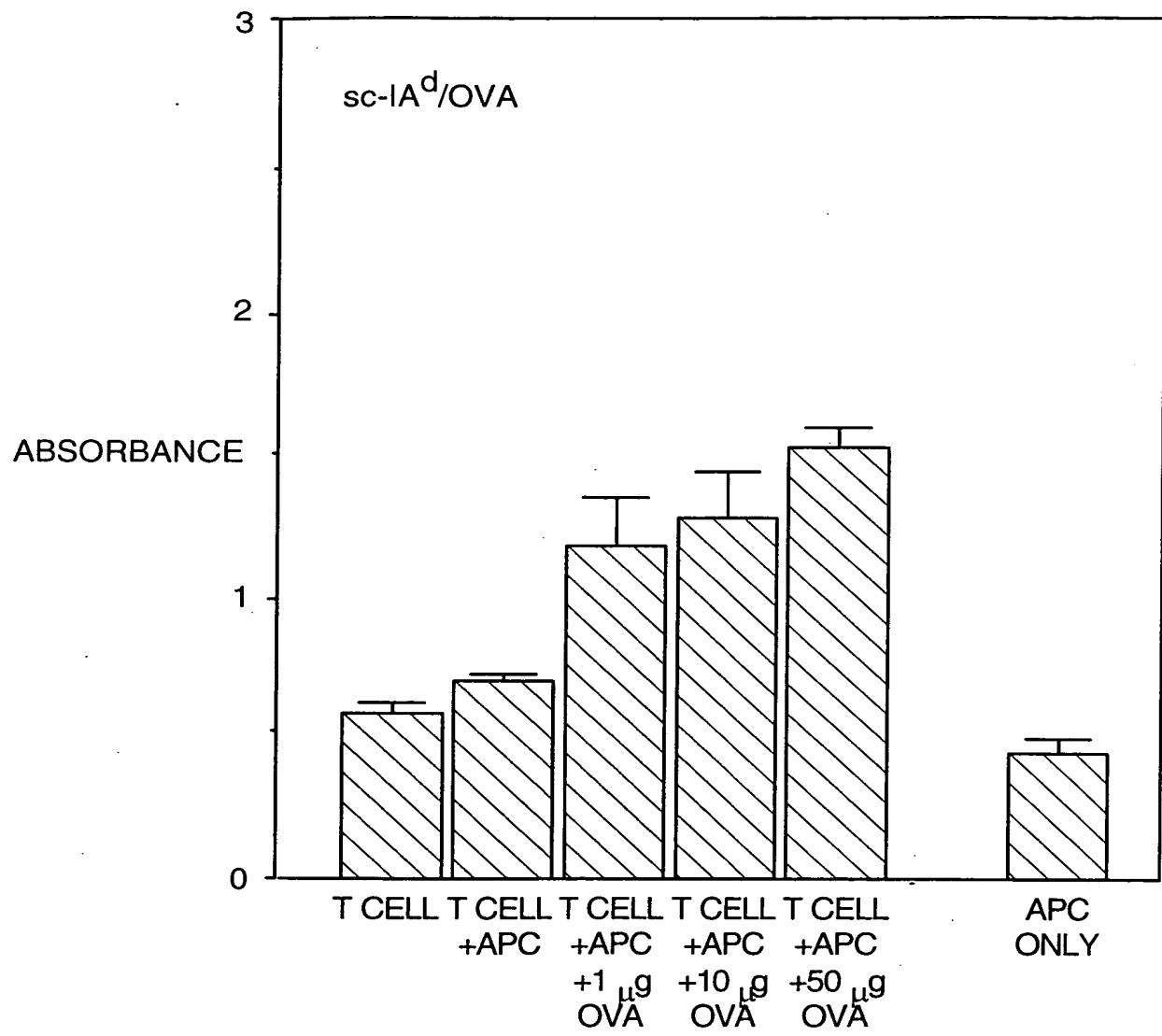


FIG. 8B

24/26

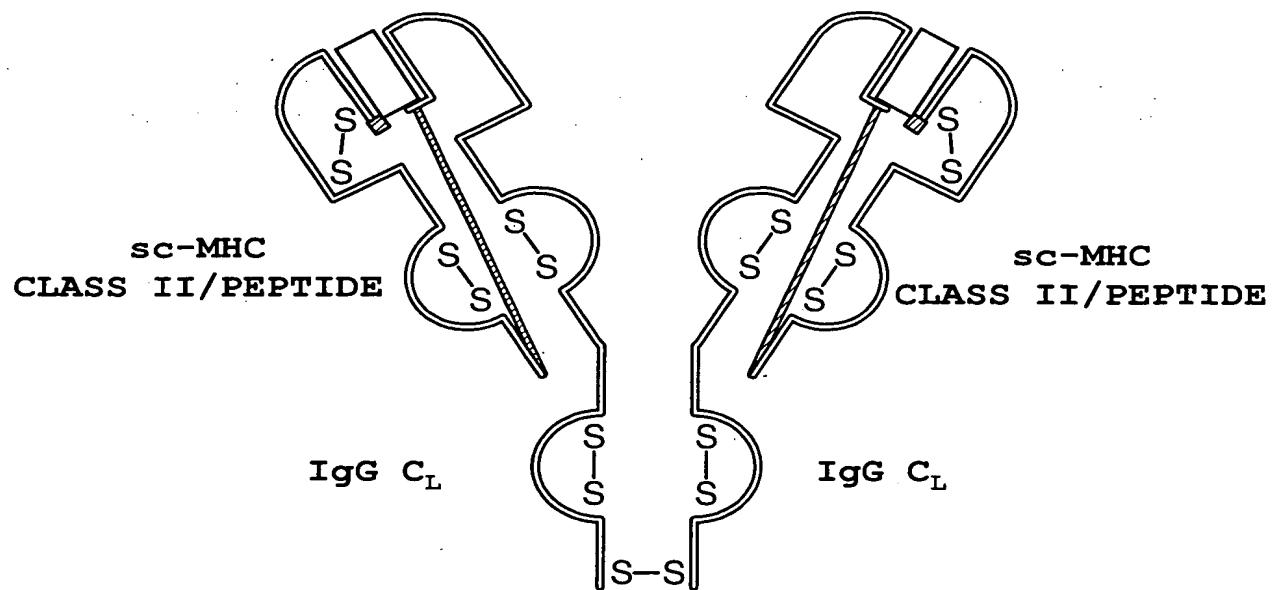


FIG. 9A

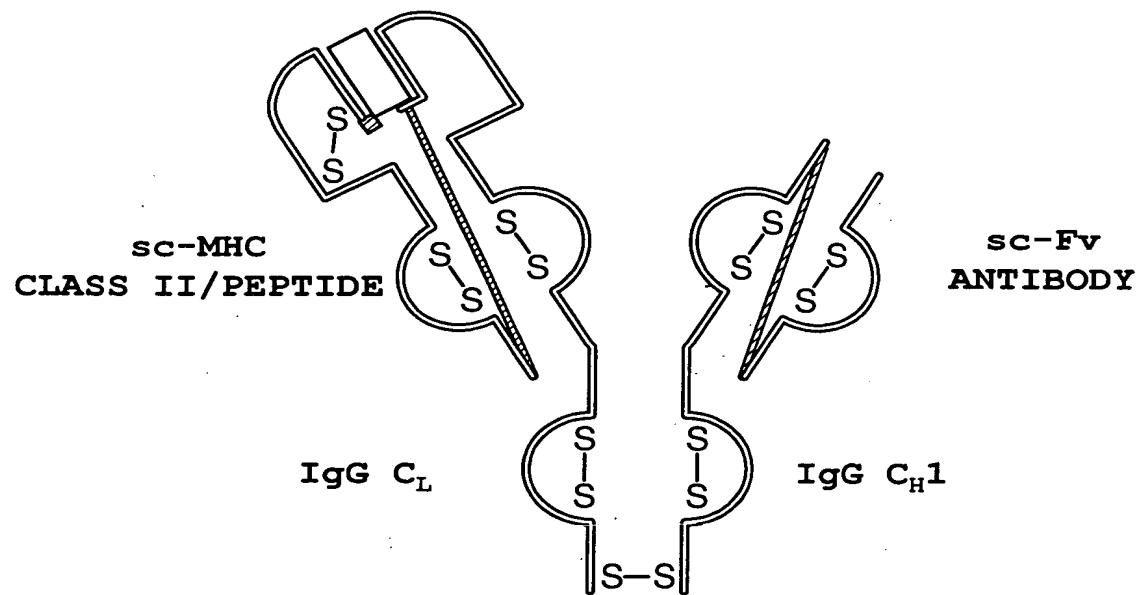


FIG. 9B

APPROVED	O. G. FIG.
BY	10/15/98
SUBCLASS	
DRAFTSMAN	

25/26

SEQ No.

CCACCATG	1
OPR132 5'-CCCCCCCAGCTTCCGGGCCACCATGGCTCTGCAGATCCCCAGC-3'	2
OPR133 5'-CCCCCCCACCTAAGGTCCCTGGGCTGCTCAGCACC-3'	3
OPR102 5'-GGGGGGGCCATGGCCGGAAACTCCGAAAGGCATTTCG-3'	4
OPR104 5'-GCGCGACTAGTCCACTCCACAGTGATGGGC-3'	5
OPR100 5'-GGGGGGGCCATGCCGAAGACGACATTGAGGCCGAC-3'	6
OPR101 5'-GCGCGACTAGTCCAGTGTTAGAACCGGGCTC-3'.	7
IADF100 5'-GGGGGGGATATCTCTCAGGCTGTTACGCTG-3'	8
IADB100 5'-GGGGGGGTTCGAAAAGTGTACTTACGGGGGCTGGAATCTCAGGTT-3'	9
OPR145 5'-GGGGGGCTCGAGTATCAAAGAACATGTGATCATC-3'	10
DR1A-B 5'-GCGCGGGATCCGTTCTGTAGTCTCTGGAGAGG-3'	11
OPR203000 5'-GATCCGAGGAAGAAGAGTACATGCCATGGAACCCGGGTGAG-3'	12
OPR203001 5'-AATTCTCACCCGGGTTCCATCGGCATGTACTCTTCTCCTCG-3'	13
DR2B-F 5'-CCCCCCGCTAGCGGAGGGGGCGGAAGCGGCCGGAGGGGGGACA CCCGACCACTGTTCTGTGGCAGCCTAACAGAGG-3'	14
DR2B-B2 5'-CCCCCCGAATTCCCCACTAGTCCATTCCACTGTGAGAGGGCTTGTC AC-3'	15
MB201806 5'-GGGGGGGCCATGGCCTACGACGAGAACCCGTGGT-3'	16
MB175959 5'-GGGGGGACTAGTCGCCGCTGCACTGTGAAGC-3'	17
MB201807 5'-GGGGGGTATGCATACGACGAGAACCCGTGGT-3'	18
MB201808 5'-GGGGGGACTAGTCCACTTCGAGGAACGTGGT-3'	19
MB201809 5'-CCTCCTGGTCTCCTCTGTGAGTGG-3'	20
MB201810 5'-CCACTCACAGAGGAGACCAGGAGG-3'	21
OPR215 5'-CCC ACC GGT TAC GAC AAC CCC GTG GTG-3'	22
OPR216 CCC CCC ATC GAT AAG TGT ACT TAC GTG GGA GAG GGC TTG GAG CAT-3'	23

FIG. 10A

APPROVED	P.O. FIG.
BY	RS
DRAFTSMAN	SUBCLASS

26/26

OVA 323-399 ISQAVHAAHAEINEAGR	26
Gd-246-261 APYSTLLPPELSETP	27
MBP (83-102) Y83 YDENPVVHFFKNIVTPRTPP	28
14 amino acid linker TSGGGGSGGGGSSS	29
EE TAG EEEEYMPMEPG	30
24 amino acid linker TSGGGGSGGGGSGGGGSGGGGSSS	31
MBP (S4-102) DENPVVHFFKNIVTPRTPP	32

FIG. 10B